

WO 2005/040191

PCT/US2004/019766

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lau, Lester F.
- (ii) TITLE OF INVENTION: Extracellular Matrix Signalling Molecules
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 - (B) STREET: 6300 Sears Tower, 233 South Wacker Drive
 - (C) CITY: Chicago
 - (D) STATE: Illinois
 - (E) COUNTRY: United States of America
 - (F) ZIP: 60606-6402
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Clough, David W.
 - (B) REGISTRATION NUMBER: 36,107
 - (C) REFERENCE/DOCKET NUMBER: 28758/33766
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 312/474-6300
 - (B) TELEFAX: 312/474-0448
 - (C) TELEX: 25-3856

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 180..1316
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (D) OTHER INFORMATION: "Mouse cyr61 cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGAGAGCGCC CCAGAGAAGC GCCTGCAATC TCTGCGCCTC CTCCGCCAGC ACCTCGAGAG 60
AAGGACACCC GCCGCCTCGG CCCTCGCCTC ACCGCACTCC GGGCGCATTT GATCCCGCTG 120

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CTCGCCGGCT TGTTGGTTCT GTGTCGCCGC GTCGCCCCG GTTCCTCTCG CGCGCCACA	179
ATG-AGC TCC AGC ACC TTC AGG ACG CTC GCT GTC GCC GTC ACC CTT CTC Met Ser Ser Ser Thr Phe Arg Thr Leu Ala Val Ala Val Thr Leu Leu 1 5 10 15	227
CAC TTG ACC AGA CTG GCG CTC TCC ACC TGC CCC GCC GCC TGC CAC TGC His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys 20 25 30	275
CCT CTG GAG GCA CCC AAG TGC GCC CCG GGA GTC GGG TTG GTC CGG GAC Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp 35 40 45	323
GGC TGC GGC TGC TGT AAG GTC TGC GCT AAA CAA CTC AAC GAG GAC TGC Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys 50 55 60	371
AGC AAA ACT CAG CCC TGC GAC CAC ACC AAG GGG TTG GAA TGC AAT TTC Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe 65 70 75 80	419
GGC GCC AGC TCC ACC GCT CTG AAA GGG ATC TGC AGA GCT CAG TCA GAA Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu 85 90 95	467
GGC AGA CCC TGT GAA TAT AAC TCC AGA ATC TAC CAA AAC GGG GAA AGC Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser 100 105 110	515
TTC CAG CCC AAC TGT AAA CAC CAG TGC ACA TGT ATT GAT GGC GCC GTG Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val 115 120 125	563
GGC TGC ATT CCT CTG TGT CCC CAA GAA CTG TCT CTC CCC AAT CTG GGC Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly 130 135 140	611
TGT CCC AAC CCC CGG CTG GTG AAA GTC AGC GGG CAG TGC TGT GAA GAG Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu 145 150 155 160	659
TGG GTT TGT GAT GAA GAC AGC ATT AAG GAC TCC CTG GAC GAC CAG GAT Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp 165 170 175	707
GAC CTC CTC GGA CTC GAT GCC TCG GAG GTG GAG TTA ACG AGA AAC AAT Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn 180 185 190	755
GAG TTA ATC GCA ATT GGA AAA GGC AGC TCA CTG AAG AGG CTT CCT GTC Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val 195 200 205	803
TTT GGC ACC GAA CCG CGA GTT CTT TTC AAC CCT CTG CAC GCC CAT GGC Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly 210 215 220	851
CAG AAA TGC ATC GTT CAG ACC ACG TCT TGG TCC CAG TGC TCC AAG AGC Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser 225 230 235 240	899
TGC GGA ACT GGC ATC TCC ACA CGA GTT ACC AAT GAC AAC CCA GAG TGC	947

Cys	Gly	Thr	Gly	Ile	Ser	Thr	Arg	Val	Thr	Asn	Asp	Asn	Pro	Glu	Cys	
CGC	CTG	GTG	AAA	GAG	ACC	CGG	ATC	TGT	GAA	GTG	CGT	CCT	TGT	GGA	CAA	995
Arg	Leu	Val	Lys	Glu	Thr	Arg	Ile	Cys	Glu	Val	Arg	Pro	Cys	Gly	Gln	
			260					265						270		
CCA	GTG	TAC	AGC	AGC	CTA	AAA	AAG	GGC	AAG	AAA	TGC	AGC	AAG	ACC	AAG	1043
Pro	Val	Tyr	Ser	Ser	Leu	Lys	Lys	Gly	Lys	Lys	Cys	Ser	Lys	Thr	Lys	
			275					280					285			
AAA	TCC	CCA	GAA	CCA	GTC	AGA	TTT	ACT	TAT	GCA	GGA	TGC	TCC	AGT	GTC	1091
Lys	Ser	Pro	Glu	Pro	Val	Arg	Phe	Thr	Tyr	Ala	Gly	Cys	Ser	Ser	Val	
			290					295				300				
AAG	AAA	TAC	CGG	CCC	AAA	TAC	TGC	GGC	TCC	TGC	GTA	GAT	GGC	CGG	TGC	1139
Lys	Lys	Tyr	Arg	Pro	Lys	Tyr	Cys	Gly	Ser	Cys	Val	Asp	Gly	Arg	Cys	
			305			310				315				320		
TGC	ACA	CCT	CTG	CAG	ACC	AGA	ACT	GTG	AAG	ATG	CGG	TTC	CGA	TGC	GAA	1187
Cys	Thr	Pro	Leu	Gln	Thr	Arg	Thr	Val	Lys	Met	Arg	Phe	Arg	Cys	Glu	
				325					330					335		
GAT	GGA	GAG	ATG	TTT	TCC	AAG	AAT	GTC	ATG	ATG	ATC	CAG	TCC	TGC	AAA	1235
Asp	Gly	Glu	Met	Phe	Ser	Lys	Asn	Val	Met	Met	Ile	Gln	Ser	Cys	Lys	
			340					345					350			
TGT	AAC	TAC	AAC	TGC	CCG	CAT	CCC	AAC	GAG	GCA	TCG	TTC	CGA	CTG	TAC	1283
Cys	Asn	Tyr	Asn	Cys	Pro	His	Pro	Asn	Glu	Ala	Ser	Phe	Arg	Leu	Tyr	
			355				360					365				
AGC	CTA	TTC	AAT	GAC	ATC	CAC	AAG	TTC	AGG	GAC	TAAGTGCCTC	CAGGGTTCCT				1336
Ser	Leu	Phe	Asn	Asp	Ile	His	Lys	Phe	Arg	Asp						
			370				375									
AGTGTGGGCT	GGACAGAGGA	GAAGCGCAAG	CATCATGGAG	ACGTGGGTGG	GCGGAGGATG											1396
AATGGTGCCT	TGCTCATTCT	TGAGTAGCAT	TAGGGTATTT	CAAACTGCC	AAGGGGCTGA											1456
TGTGGACGGA	CAGCAGCGCA	GCCG														1480

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (D) OTHER INFORMATION: "Mouse Cyr61 amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Ser	Ser	Thr	Phe	Arg	Thr	Leu	Ala	Val	Ala	Val	Thr	Leu	Leu	
1				5					10					15		
His	Leu	Thr	Arg	Leu	Ala	Leu	Ser	Thr	Cys	Pro	Ala	Ala	Cys	His	Cys	
				20				25					30			
Pro	Leu	Glu	Ala	Pro	Lys	Cys	Ala	Pro	Gly	Val	Gly	Leu	Val	Arg	Asp	

35 40 45
 Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys
 50 55 60
 Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe
 65 70 75 80
 Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu
 85 90 95
 Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser
 100 105 110
 Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val
 115 120 125
 Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly
 130 135 140
 Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu
 145 150 155 160
 Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp
 165 170 175
 Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn
 180 185 190
 Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val
 195 200 205
 Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly
 210 215 220
 Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser
 225 230 235 240
 Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys
 245 250 255
 Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln
 260 265 270
 Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys
 275 280 285
 Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val
 290 295 300
 Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys
 305 310 315 320
 Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu
 325 330 335
 Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys
 340 345 350
 Cys Asn Tyr Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr
 355 360 365
 Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp

370

375

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 124..1266

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: "Human cyr61 cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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GGGCGGGCCC ACCGCGACAC CGCGCCGCCA CCCCAGCCCC GCTGCGCACG GCCTGTCCGC      60
TGCACACCAG CTGTGTTGGCG TCCTCGTCGC CGCGCTCGCC CCGGGCTACT CCTGCGCGCC      120
ACA ATG AGC TCC CGC ATC GCC AGG GCG CTC GCC TTA GTC GTC ACC CTT      168
  Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu
    1             5             10             15
CTC CAC TTG ACC AGG CTG GCG CTC TCC ACC TGC CCC GCT GCC TGC CAC      216
Leu His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His
              20             25             30
TGC CCC CTG GAG GCG CCC AAG TGC GCG CCG GGA GTC GGG CTG GTC CGG      264
Cys Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg
              35             40             45
GAC GGC TGC GGC TGC TGT AAG GTC TGC GCC AAG CAG CTC AAC GAG GAG      312
Asp Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp
              50             55             60
TGC AGC AAA ACG CAG CCC TGC GAC CAC ACC AAG GGG CTG GAA TGC AAC      360
Cys Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn
              65             70             75
TTC GGC GCC AGC TCC ACC GCT CTG AAG GGG ATC TGC AGA GCT CAG TCA      408
Phe Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser
              80             85             90             95
GAG GGC AGA CCC TGT GAA TAT AAC TCC AGA ATC TAC CAA AAC GGG GAA      456
Glu Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu
              100            105            110
AGT TTC CAG CCC AAC TGT CAA CAT CAG TGC ACA TGT ATT GAT GGC GCC      504
Ser Phe Gln Pro Asn Cys Gln His Gln Cys Thr Cys Ile Asp Gly Ala
              115            120            125
GTG GGC TGC ATT CCT CTG TGT CCC CAA GAA CTA TCT CTC CCC AAC TTG      552
Val Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu
              130            135            140
GGC TGT CCC AAC CCT CGG CTG GTC AAA GTT ACC GGG CAG TGC TGC GAG      600

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Gly	Cys	Pro	Asn	Pro	Arg	Leu	Val	Lys	Val	Thr	Gly	Gln	Cys	Cys	Glu	
145						150					155					
GAG Glu 160	TGG Trp	GTC Val	TGT Cys	GAC Asp	GAG Glu	GAT Asp	AGT Ser	ATC Ile	AAG Lys	GAC Asp	CCC Pro	ATG Met	GAG Glu	GAC Asp	CAG Gln	648
GAC Asp	GGC Gly	CTC Leu	CTT Leu	GGC Gly	AAG Lys	GAG Glu	CTG Leu	GGA Gly	TTC Phe	GAT Asp	GCC Ala	TCC Ser	GAG Glu	GTG Val	GAG Glu	696
TTG Leu	ACG Thr	AGA Arg	AAC Asn	AAT Asn	GAA Glu	TTG Leu	ATT Ile	GCA Ala	GTT Val	GGA Gly	AAA Lys	GGC Gly	AGA Arg	TCA Ser	CTG Leu	744
AAG Lys	CGG Arg	CTC Leu	CCT Pro	GTT Val	TTT Phe	GGA Gly	ATG Met	GAG Glu	CCT Pro	CGC Arg	ATC Ile	CTA Leu	TAC Tyr	AAC Asn	CCT Pro	792
TTA Leu	CAA Gln	GGC Gly	CAG Gln	AAA Lys	TGT Cys	ATT Ile	GTT Val	CAA Gln	ACA Thr	ACT Thr	TCA Ser	TGG Trp	TCC Ser	CAG Gln	TGC Cys	840
TCA Ser	AAG Lys	ACC Thr	TGT Cys	GGA Gly	ACT Gly	GGT Ile	ATC Ile	TCC Ser	ACA Thr	CGA Arg	GTT Val	ACC Thr	AAT Asn	GAC Asp	AAC Asn	888
CCT Pro	GAG Glu	TGC Cys	CGC Arg	CTT Leu	GTG Val	AAA Lys	GAA Glu	ACC Thr	CGG Arg	ATT Ile	TGT Cys	GAG Glu	GTG Val	CGG Arg	CCT Pro	936
TGT Cys	GGA Gly	CAG Gln	CCA Pro	GTG Val	TAC Tyr	AGC Ser	AGC Ser	CTG Leu	AAA Lys	AAG Lys	GGC Gly	AAG Lys	AAA Lys	TGC Cys	AGC Ser	984
AAG Lys	ACC Thr	AAG Lys	AAA Lys	TCC Ser	CCC Pro	GAA Glu	CCA Pro	GTC Val	AGG Arg	TTT Phe	ACT Thr	TAC Tyr	GCT Ala	GGA Gly	TGT Cys	1032
TTG Leu	AGT Ser	GTG Val	AAG Lys	AAA Lys	TAC Tyr	CGG Arg	CCC Pro	AAG Lys	TAC Tyr	TGC Cys	GGT Gly	TCC Ser	TGC Cys	GTG Val	GAC Asp	1080
GGC Gly	CGA Arg	TGC Cys	TGC Cys	ACG Thr	CCC Pro	CAG Gln	CTG Leu	ACC Thr	AGG Arg	ACT Thr	GTG Val	AAG Lys	ATG Met	CGG Arg	TTC Phe	1128
CGC Arg	TGC Cys	GAA Glu	GAT Asp	GGG Gly	GAG Glu	ACA Thr	TTT Phe	TCC Ser	AAG Lys	AAC Asn	GTC Val	ATG Met	ATG Met	ATC Ile	CAG Gln	1176
TCC Ser	TGC Cys	AAA Lys	TGC Cys	AAC Asn	TAC Tyr	AAC Asn	TGC Cys	CCG Pro	CAT His	GCC Ala	AAT Asn	GAA Glu	GCA Ala	GCG Ala	TTT Phe	1224
CCC Pro	TTC Phe	TAC Tyr	AGG Arg	CTG Leu	TTC Phe	AAT Asn	GAC Asp	ATT Ile	CAC His	AAA Lys	TTT Phe	AGG Arg	GAC Asp			1266
TAAATGCTAC	CTGGGTTTCC	AGGGCACACC	TAGACAAACA	AGGGAGAAGA	GTGTCAGAAT											1326
CAGAATCATG	GAGAAAATGG	GCGGGGGTGG	TGTGGGTGAT	GGGACTCATT	G TAGAAAGGA											1386

AGCCTTCTCA TTCTTGAGGA GCATTAAGGT AT

1418

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (D) OTHER INFORMATION: "Human Cyr61 amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu Leu
 1           5           10           15
His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys
 20           25           30
Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp
 35           40           45
Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys
 50           55           60
Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe
 65           70           75           80
Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu
 85           90           95
Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser
100          105          110
Phe Gln Pro Asn Cys Gln His Gln Cys Thr Cys Ile Asp Gly Ala Val
115          120          125
Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly
130          135          140
Cys Pro Asn Pro Arg Leu Val Lys Val Thr Gly Gln Cys Cys Glu Glu
145          150          155          160
Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln Asp
165          170          175
Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu Leu
180          185          190
Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Arg Ser Leu Lys
195          200          205
Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro Leu
210          215          220
Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser
225          230          235          240
Lys Thr Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro

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245 250 255
 Glu Cys Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys
 260 265 270
 Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys
 275 280 285
 Thr Lys Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Leu
 290 295 300
 Ser Val Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly
 305 310 315 320
 Arg Cys Cys Thr Pro Gln Leu Thr Arg Thr Val Lys Met Arg Phe Arg
 325 330 335
 Cys Glu Asp Gly Glu Thr Phe Ser Lys Asn Val Met Met Ile Gln Ser
 340 345 350
 Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe Pro
 355 360 365
 Phe Tyr Arg Leu Phe Asn Asp Ile His Lys Phe Arg Asp
 370 375 380

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (D) OTHER INFORMATION: "Fispl2 cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCGCC GACAACCCCA GACGCCACCG CCTGGAGCGT CCAGACACCA ACCTCCGCCC 60
 CTGTCCGAAT CCAGGCTCCA GCCGCGCCTC TCGTCGCCTC TGCACCCTGC TGTGCATCCT 120
 CCTACCGCGT CCCGATCATG CTCGCCTCCG TCGCAGGTCC CATCAGCCTC GCCTTGGTGC 180
 TCCTCGCCCT CTGCACCCGG CCTGCTACGG GCCAGGACTG CAGCGCGCAA TGTCAGTGCG 240
 CAGCCGAAGC AGCGCCGCAC TGCCCCGCCG GCGTGAGCCT GGTGCTGGAC GGCTGCGGCT 300
 GCTGCCGCGT CTGCGCCAAG CAGCTGGGAG AACTGTGTAC GGAGCGTGAC CCCTGCGACC 360
 CACACAAGGG CCTCTTCTGC GATTTCGGCT CCCCCGCAA CCGCAAGATT GGAGTGTGCA 420
 CTGCCAAAGA TGGTGACCC TGTGTCTTCG GTGGGTGCGT GTACCGCAGC GGTGAGTCCT 480
 TCCAAAGCAG CTGCAATAC CAATGCACTT GCCTGGATGG GGCCGTGGGC TGCCTGCCCC 540
 TATGCAGCAT GGACGTGCGC CTGCCCAGCC CTGACTGCCC CTTCCCGAGA AGGGTCAAGC 600
 TGCTTGGGAA ATGCTGCAAG GAGTGGGTGT GTGACGAGCC CAAGGACCGC ACAGCAGTTG 660

GCCCTGCCCT AGCTGCCTAC CGACTGGAAG ACACATTTGG CCCAGACCCA ACTATGATGC	720
GAGCCAACTG CCTGGTCCAG ACCACAGAGT GGAGCGCCTG TTCTAAGACC TGTGGAATGG	780
GCATCTCCAC CCGAGTTACC AATGACAATA CCTTCTGCAG ACTGGAGAAG CAGAGCCGCC	840
TCTGCATGGT CAGGCCCTGC GAAGCTGACC TGGAGGAAAA CATTAGAAG GGCAAAAAGT	900
GCATCCGGAC ACCTAAAATC GCCAAGCCTG TCAAGTTTGA GCTTCTGGC TGCACCACTG	960
TGAAGACATA CAGGGCTAAG TTCTGCGGG TGTGCACAGA CGGCCCTGC TGCACACCGC	1020
ACAGAACCAC CACTCTGCCA GTGGAGTTCA AATGCCCGA TGGCGAGATC ATGAAAAAGA	1080
ATATGATGTT CATCAAGACC TGTGCCTGCC ATTACAACTG TCCTGGGGAC AATGACATCT	1140
TTGAGTCCCT GTACTACAGG AAGATGTACG GAGACATGGC GTAAAGCCAG GAAGTAAGGG	1200
ACACGAACTC ATTAGACTAT AACTTGAAGT GAGTTGCATC TCATTTTCTT CTGTAAAAAC	1260
AATTACAGTA GCACATTAAT TTAAATCTGT GTTTTAACT ACCGTGGGAG GAACTATCCC	1320
ACCAAAGTGA GAACGTTATG TCATGGCCAT ACAAGTAGTC TGTC AACCTC AGACACTGGT	1380
TTGAGACAG TTTACACTTG ACAGTTGTTT ATTAGCGCAC AGTGCCAGAA CGCACACTGA	1440
GGTGAGTCTC CTGGAACAGT GGAGATGCCA GGAGAAAGAA AGACAGGTAC TAGCTGAGGT	1500
TATTTTAAAA GCAGCAGTGT GCCTACTTTT TGGAGTGTAA CCGGGGAGGG AAATTATAGC	1560
ATGCTTGCAG ACAGACCTGC TCTAGCGAGA GCTGAGCATG TGTCCTCCAC TAGATGAGGC	1620
TGAGTCCAGC TGTTCTTTAA GAACAGCAGT TTCAGCCTCT GACCATTCTG ATTCCAGTGA	1680
CACTTGTGAG GAGTCAGAGC CTTGTCTGTT AGACTGGACA GCTTGTGGCA AGTAAGTTTG	1740
CCTGTAACAA GCCAGATTTT TATTGATATT GTAAATATTG TGGATATATA TATATATATA	1800
TATATTTGTA CAGTTATCTA AGTTAATTTA AAGTCATTG TTTTGTGTTT AAGTGCTTTT	1860
GGGATTTTAA ACTGATAGCC TCAAACTCCA AACACCATAG GTAGGACACG AAGCTTATCT	1920
GTGATTCAAA ACAAGGAGA TACTGCAGTG GGAATTGTGA CCTGAGTGAC TCTCTGTCAG	1980
AACAAACAAA TGCTGTGCAG GTGATAAAGC TATGTATTGG AAGTCAGATT TCTAGTAGGA	2040
AATGTGGTCA AATCCCTGTT GGTGAACAAA TGGCCTTTAT TAAGAAATGG CTGGCTCAGG	2100
GTAAGGTCCG ATTCCTACCA GGAAGTGCTT GCTGCTTCTT TGATTATGAC TGGTTTGGGG	2160
TGGGGGGCAG TTTATTTGTT GAGAGTGTGA CCAAAAGTTA CATGTTTGCA CCTTTCTAGT	2220
TGAAAATAAA GTATATATAT ATTTTATATA TGAAAAAAA GGAATTC	2267

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: misc feature

(D) OTHER INFORMATION: "Fispl2 amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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Met Leu Ala Ser Val Ala Gly Pro Ile Ser Leu Ala Leu Val Leu Leu
 1           5           10           15
Ala Leu Cys Thr Arg Pro Ala Thr Gly Gln Asp Cys Ser Ala Gln Cys
          20           25           30
Gln Cys Ala Ala Glu Ala Ala Pro His Cys Pro Ala Gly Val Ser Leu
          35           40           45
Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu Gly
 50           55           60
Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu Phe
 65           70           75           80
Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr Ala
          85           90           95
Lys Asp Gly Ala Pro Cys Val Phe Gly Gly Ser Val Tyr Arg Ser Gly
          100          105          110
Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp Gly
          115          120          125
Ala Val Gly Cys Val Pro Leu Cys Ser Met Asp Val Arg Leu Pro Ser
          130          135          140
Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys Cys
          145          150          155          160
Lys Glu Trp Val Cys Asp Glu Pro Lys Asp Arg Thr Ala Val Gly Pro
          165          170          175
Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro Thr
          180          185          190
Met Met Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala Cys
          195          200          205
Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp Asn
          210          215          220
Thr Phe Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg Pro
          225          230          235          240
Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys Ile
          245          250          255
Arg Thr Pro Lys Ile Ala Lys Pro Val Lys Phe Glu Leu Ser Gly Cys
          260          265          270
Thr Ser Val Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr Asp
          275          280          285
Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu Phe
          290          295          300

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Lys Cys Pro Asp Gly Glu Ile Met Lys Lys Asn Met Met Phe Ile Lys
 305 310 315 320
 Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe Glu
 325 330 335
 Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
 340 345

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2075 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: "CTGF cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

CCCCGCCGAC AGCCCCGAGA CGACAGCCCG GCGCGTCCCG GTCCCCACCT CCGACCACCG      60
CCAGCGCTCC AGGCCCCGCG CTCCCCGCTC GCCGCCACCG CGCCCTCCGC TCCGCCGCA      120
GTGCCAACCA TGACCGCCGC CAGTATGGGC CCCGTCCGCG TCGCCTTCGT GGTCTCTCTC      180
GCCCTCTGCA GCCGGCCGGC CGTEGGCCAG AACTGCAGCG GGCCGTGCCG GTGCCCGGAC      240
GAGCCGGCGC CGCGCTGCCC GGCGGGCGTG AGCCTCGTGC TGGACGGCTG CGGCTGCTGC      300
CGCGTCTGCG CCAAGCAGCT GGGCGAGCTG TGACCCGAGC GCGACCCCTG CGACCCGCAC      360
AAGGGCCTCT TCTGTGACTT CGGCTCCCCG GCCAACCACA AGATCGGCGT GTGCACCGCC      420
AAAGATGGTG CTCCCTGCAT CTTCCGTGGT ACGGTGTACC GCAGCGGAGA GTCCTTCCAG      480
AGCAGCTGCA AGTACCAAGT CACGTGCCTG GACGGGGCGG TGGGCTGCAT GCCCCTGTGC      540
AGCATGGACG TTCGTCTGCC CAGCCCTGAC TGCCCTTCC CGAGGAGGGT CAAGCTGCCC      600
GGGAAATGCT GCGAGGAGTG GGTGTGTGAC GAGCCCAAGG ACCAAACCGT GGTGGGCCT      660
GCCCTCGCGG CTTACCGACT GGAAGACACG TTTGGCCAG ACCCAACTAT GATTAGAGCC      720
AACTGCCTGG TCCAGACCAC AGAGTGGAGC GCCTGTTCCTA AGACCTGTGG GATGGGCATC      780
TCCACCCGGG TTACCAATGA CAACGCCTCC TGCAGGCTAG AGAAGCAGAG CCGCCTGTGC      840
ATGGTCAGGC CTTGCGAAGC TGACCTGGAA GAGAACATTA AGAAGGGCAA AAAGTGCATC      900
CGTACTCCCA AAATCTCCAA GCCTATCAAG TTTGAGCTTT CTGGCTGCAC CAGCATGAAG      960
ACATACCGAG CTAAATTCTG TGGAGTATGT ACCGACGGCC GATGCTGCAC CCCCCACAGA     1020
ACCACCACCC TGCCGGTGGG GTTCAAGTGC CCTGACGGCG AGGTCATGAA GAAGAACATG     1080
ATGTTTCATCA AGACCTGTGC CTGCCATTAC AACTGTCCCG GAGACAATGA CATCTTTGAA     1140

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TCGCTGTACT ACAGGAAGAT GTACGGAGAC ATGGCATGAA GCCAGAGAGT GAGAGACATT 1200
 AACTCATTAG ACTGGAACCT GAACTGATTC ACATCTCATT TTTCCGTAAA AATGATTTCA 1260
 GTAGCACAAG TTATTTAAAT CTGTTTTTCT AACTGGGGGA AAAGATTCCC ACCCAATTCA 1320
 AAACATTGTG CCATGTCAAA CAAATAGTCT ATCTTCCCA GACACTGGTT TGAAGAATGT 1380
 TAAGACTTGA CAGTGGAACT ACATTAGTAC ACAGCACCAG AATGTATATT AAGGTGTGGC 1440
 TTTAGGAGCA GTGGGAGGGT ACCGGCCCCG TTAGTATCAT CAGATCGACT CTTATACGAG 1500
 TAATATGCCT GCTATTGAA GTGTAATTGA GAAGGAAAAT TTTAGCGTGC TCACTGACCT 1560
 GCCTGTAGCC CCAGTGACAG CTAGGATGTG CATTCTCCAG CCATCAAGAG ACTGAGTCAA 1620
 GTTGTTCCTT AAGTCAGAAC AGCAGACTCA GCTCTGACAT TCTGATTCGA ATGACACTGT 1680
 TCAGGAATCG GAATCCTGTC GATTAGACTG GACAGCTTGT GGCAAGTGAA TTGCCTGTA 1740
 ACAAGCCAGA TTTTITAAAA TTTATATTGT AAATATTGTG TGTGTGTGTG TGTGTGTATA 1800
 TATATATATA TATGTACAGT TATCTAAGTT AATTTAAAGT TGTGTGTGCC TTTTATTTT 1860
 TGTTTTTAAT GCTTTGATAT TTCAATGTTA GCCTCAATTT CTGAACACCA TAGGTAGAAT 1920
 GTAAAGCTTG TCTGATCGTT CAAAGCATGA AATGGATACT TATATGGAAA TTCTGCTCAG 1980
 ATAGAATGAC AGTCCGTCOA AACAGATTGT TTGCAAAGGG GAGGCATCAG TGTCTTGGCA 2040
 GGCTGATTTT TAGGTAGGAA ATGTGGTAGC TCACG 2075

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: "CTGF amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val Val Leu
 1 5 10 15
 Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser Gly Pro
 20 25 30
 Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser
 35 40 45
 Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu
 50 55 60
 Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu
 65 70 75 80

Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr
 85 90 95
 Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser
 100 105 110
 Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp
 115 120 125
 Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro
 130 135 140
 Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys
 145 150 155 160
 Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly
 165 170 175
 Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro
 180 185 190
 Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala
 195 200 205
 Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp
 210 215 220
 Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg
 225 230 235 240
 Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys
 245 250 255
 Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly
 260 265 270
 Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr
 275 280 285
 Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu
 290 295 300
 Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile
 305 310 315 320
 Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe
 325 330 335
 Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
 340 345

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGGATCTGT GACGAGCCCA AGGAC

25

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGAATTCGA CCAGGCAGTT GGCTCG

26

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGGGATCCTG TGATGAAGAC AGCATT

26

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGGAATTCAA CGATGCATT CTGGCC

26

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asp Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp
1 5 10 15
Cys Ser Lys Thr Gln
20

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val Gly Cys
1 5 10 15
Ile Pro Leu Cys Pro
20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser Cys Gly
1 5 10 15
Thr Gly Ile Ser Thr Arg Val Thr
20

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys Arg Leu Val Lys
1 5 10 15
Glu Thr Arg Ile Cys Glu Val Arg Pro Cys
20 25

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys Cys Thr Pro Leu Gln
1 5 10 15
Thr Arg Thr Val Lys
20

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